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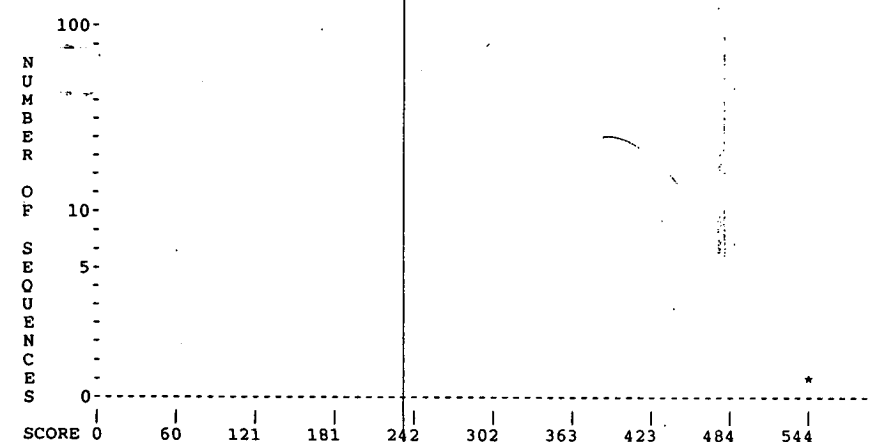
FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-831-805a-20.res made by jdelaval on Thu 8 May 103 6:06:21-PDT.

Query sequence being compared:US-09-831-805A-20 (1-917)
Number of sequences searched: 1
Number of scores above cutoff: 1

Results of the initial comparison of US-09-831-805A-20 (1-917) with:
File : y14736.seq



PARAMETERS

Similarity matrix	Unitary	K-tuple	4
Mismatch penalty	1	Joining penalty	30
Ga[illegible]alty	1.00	Window size	32
G[illegible]e penalty	0.33		
Cu[illegible]score	0		
Randomization group	0		

SEARCH STATISTICS

Scores:	Mean	Median	Standard Deviation
	544	0	0.00

Times:	CPU	Total Elapsed
	00:00:00.00	00:00:00.00

Number of residues: 938
Number of sequences searched: 1
Number of scores above cutoff: 1

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:

Sequence Name	Description	Length	Init. Score	Opt. Score	Sig.	Frame
1. y14736	TOIG of: y14736 check: 615	938	544	878	0.00	0

1. US-09-831-805A-20 (1-917)
y14736 TOIG of: y14736 check: 615 from: 1 to: 938

TOIG of: y14736 check: 615 from: 1 to: 938

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LOCUS       HSIGG1KL                938 bp    mRNA    linear   PRI 19-AUG-1998
DEFINITION  Homo sapiens mRNA for immunoglobulin kappa light chain.
ACCESSION   Y14736
VERSION     Y14736.1  GI:2765422
KEYWORDS    constant region; IgG1; immunoglobulin; kappa light chain; variable
            region.
SOURCE      Homo sapiens.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 938)
  AUTHORS   Paterson,T., Innes,J., McMillan,L., Downing,I. and Carter,M.C.
  TITLE     Variation in IgG1 heavy chain allotype does not contribute to
            differences in biological activity of two human anti-Rhesus (D)
            monoclonal antibodies
  JOURNAL   Immunotechnology 4 (1), 37-47 (1998)
  MEDLINE   98326459
   PUBMED   9661813
REFERENCE   2  (bases 1 to 938)
  AUTHORS   Paterson,T.
  TITLE     Direct Submission
  JOURNAL   Submitted (03-SEP-1997) T. Paterson, National Science Laboratory,
            Scottish Nat. Blood Transfusion Service, 12 Bristo Place,
            Edinburgh, EH1 1EZ, Scotland, UK
COMMENT     Cell line reference: McCann Carter M.C. et al (1993), Transfusion
            Medicine, 3, 187-194.
FEATURES             Location/Qualifiers
     source          1. .938
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /cell_line="human /mouse (NS-0) hetero-hybridoma cell line
                     ESD-1 (THERAD 03)"
     gene            15. .725
                     /gene="IgG1K"
     CDS             15. .725
                     /gene="IgG1K"
                     /codon_start=1
                     /product="immunoglobulin kappa light chain"
                     /protein_id="CAA75031.1"
                     /db_xref="GI:2765423"
                     /translation="MDMRVPAQLLGLLLLWLRGARCDIQLTQSPSSLSAAVGDRVTIA
                     CRASQSIADYLNWYQQKPGKAPKLLIYGSSSLQSGVPSRFSGSGSGTDFTLSISSLQP
                     GDFATYYCQQSHTSPFTFGGGTKVQMKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNN
                     FYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEV
                     THQGLSSPVTKSFNRGEC"
     sig_peptide     15. .80
                     /gene="IgG1K"
     mat_peptide     81. .722
                     /gene="IgG1K"
                     /product="immunoglobulin kappa light chain"
     V_region        81. .401
                     /gene="IgG1K"
                     /product="immunoglobulin kappa light chain variable
                     region"
     C_region        402. .725
                     /gene="IgG1K"
                     /product="immunoglobulin kappa light chain constant
                     region"
BASE COUNT      237 a    274 c    218 g    209 t
ORIGIN

Y14736  Length: 938  May 8, 2003 06:02  Type: N  Check: 615  ..
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Initial Score    =    544  Optimized Score  =    878  Significance =  0.00
Residue Identity =    95%  Matches          =    881  Mismatches   =    33
Gaps             =      4  Conservative Substitutions               =     0

    X       10        20        30        40        50        60        70
     GTCAGGACACAGCATGGACATGAGGGTCCCCGCTCAGCTCCTGGGGCTCCTGCTACTCTGGCTCCGAGGTG
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    GGTCAGGACACAGCATGGACATGAGGGTCCCCGCTCAGCTCCTGGGGCTCCTGCTACTCTGGCTCCGAGGTG
     X      10        20        30        40        50        60        70

           80        90       100       110       120       130       140
    CCAGATGTGACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCA
    |||||||||||||||| ||||||||||||||||||||||||||||| ||||||||||||||||||||||||
    CCAGATGTGACATCCAGTTGACCCAGTCTCCATCCTCCCTGTCTGCAGCTGTAGGAGACAGAGTCACCATCG
           80        90       100       110       120       130       140

       150       160       170       180       190       200       210
    CTTGCCGGGCAGGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAGC
    |||||||||| |||||||||| |  ||||||||||||||||||||||||||||||||||||||||||| |
    GCCGGGCAAGTCAGAGCATTGCCGACTATTTAAATTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAAC
        50        160       170       180       190       200       210

      220       230       240       250       260       270       280
    TCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTTCAGTGGCAGTGGATCTGGGACAG
    |||||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    TCCTGATCTATGGTTCATCCAGTTTGCAAAGCGGGGTCCCATCAAGGTTCAGTGGCAGTGGATCTGGGACAG
     220       230       240       250       260       270       280

    290       300       310       320       330       340       350
    ATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAGATTTTGCAACTTACTACTGTCAACAGAGTTACAGTA
    |||||||||||| |||||||||||| |||||| |||||||||||||||||||||||||||| ||| |
    ATTTCACTCTCTCCATCAGCAGTCTACAACCTGGAGATTTTGCAACTTACTACTGTCAACAGAGTCACACTT
  290       300       310       320       330       340       350       360

  360       370       380       390       400       410       420       430
    CCCCTCCGATCACCTTCGGCCAAGGGACACGACTGGAGATTAAACGAACTGTGGCTGCACCATCTGTCTTCA
    |||||    |||| || |||  ||||||      || |||| || ||||||||||||||||||||||||||
    CCCCT---TTCACTTTTGGCGGAGGGACCAAGGTGCAGATGAAGCGAACTGTGGCTGCACCATCTGTCTTCA
              370       380       390       400       410       420

         440       450       460       470       480       490       500
    TCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATC
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    TCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATC
  430       440       450       460       470       480       490       500

       510       520       530       540       550       560       570
    CCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTCACAG
    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
     AGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTCACAG
         510       520       530       540       550       560       570

       580       590       600       610       620       630       640
    AGCAGGACAGCAAGGACAGCACCTACAGCCTCAGCAGCACCCTGACGCTGAGCAAAGCAGACTACGAGAAAC
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    AGCAGGACAGCAAGGACAGCACCTACAGCCTCAGCAGCACCCTGACGCTGAGCAAAGCAGACTACGAGAAAC
        580       590       600       610       620       630       640

    650       660       670       680       690       700       710
    ACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAG
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    ACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAG
      650       660       670       680       690       700       710

  720       730       740       750       760       770       780       790
    AGTGTTAGAGGGAGAAGTGCCCCCACCTGCTCCTCAGTTCCAGCCTGACCCCCTCCCATCCTTTGGCCTCTG
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    AGTGTTAGAGGGAGAAGTGCCCCCACCTGCTCCTCAGTTCCAGCCTGACCCCCTCCCATCCTTTGGCCTCTG
    720       730       740       750       760       770       780

          800       810       820       830       840       850       860
    ACCCTTTTTCCACAGGGGACCTACCCCTATTGCGGTCCTCCAGCTCATCTTTCACCTCACCCCCCTCCTCCT
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    ACCCTTTTTCCACAGGGGACCTACCCCTATTGCGGTCCTCCAGCTCATCTTTCACCTCACCCCCCTCCTCCT
  790       800       810       820       830       840       850       860

       870       880       890       900       910       X
    CCTTGGCTTTAATTATGCTAATGTTGGAGGAGAATGAATAAATAAAGTG-ATCGA
    |||||||||||||||||||||||||||||||||||||||||||||||| |||
    CCTTGGCTTTAATTATGCTAATGTTGGAGGAGAATGAATAAATAAAGTGAATCTTTGCACCTAAAAAAAAAA
       870       880       890       900       910       X 920       930

    AAAAA
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